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Fig. 1:

	1		56
I16 human	MnsFStsaFgPVAFsLGLLLVlpaAFPapvpggeDskDvaaPhRQpLTsSErIDkq		
I16 mouse	MkFLSaRdFhPVAf.LGLMLVttTAFptsqvrRGDFtEdttPnRpVyTtSQ.VGgl		
I16 hhv8	McWFKlWsL....LlVGsLLVsgT.....RGKlpDapefeKDLLi.....qr		
Consensus	* * **		
	57		112
I16 human	IrYILdgIsaLRKEtCNKSnmCeSskeALAENNLnLPkMaEkDGCFQsGFNEEtCL		
I16 mouse	IthVLWeIvEMRKELCNgnsdCmnnDDALAENNLKLPeIqrndGCYQtGYNQEIcL		
I16 hhv8	LnWMLWvIdEcFRDLCyRtGIckGilEpaAifhLKLPaIndtDhCgliGFNetsCL		
Consensus	* * * * * * ** * * * **		
		^ ^ ^ ^	
	113		168
I16 human	VKIitGLLEFEVYLEYLqNrF.EsSeEqARaVQMSTkvLIQFLQkkakNLdaIttP		
I16 mouse	LKIssGLLEYhsYLEYMknNlkDnkKdkARVLQrdTeTLIHIFnQEVKDLhKIvlP		
I16 hhv8	kKLadGFFEFEVlFkFLtteF.GkSvinvdVMELLTKTLgwdIQEELnkLtKthys		
Consensus	* * *	* *	*
	169		223
I16 human	dPttnASLLtKLQAQnQWLqdmTtHLILRSFkeFLqssLRaLRQM.....		
I16 mouse	tPiSnAlLtDKLESQKEWLRtkTiQFILKSLEEFLkvtLRstRQt.....		
I16 hhv8	pPkfDrGllGRlQGlgKywVRhfafyVLsaMEkfaggaVRvLdsIpdvtpdvhdK		
Consensus	* * * * * * *		

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Fig. 2:

SEQUENCE LISTING

1. Sequence characteristics:
 - 1.1. Length: 612 base pairs
 - 1.2. Type: Nucleic Acid
 - 1.3. Strandedness: Double stranded
 - 1.4. Topology: Linear
2. Molecule type: Genomic DNA
3. Description: Human herpesvirus 8 interleukin-6 gene
4. Hypothetical: No
5. Anti-sense: No
6. Original source: Kaposi Sarkoma from HIV positive donor
7. Organism: Human herpesvirus 8

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1	ATG	TGC	TGG	TTC	AAG	TTG	TGG	TCT	CTC	TTG	CTG	GTC	GGT	TCA	CTG
1	M	C	W	F	K	L	W	S	L	L	L	V	G	S	L
1	Met	Cys	Trp	Phe	Lys	Leu	Trp	Ser	Leu	Leu	Leu	Val	Gly	Ser	Leu
46	CTG	GTA	TCT	GGA	ACG	CGG	GGC	AAG	TTG	CCG	GAC	GCC	CCC	GAG	TTT
16	L	V	S	G	T	R	G	K	L	P	D	A	P	E	F
16	Leu	Val	Ser	Gly	Thr	Arg	Gly	Lys	Leu	Pro	Asp	Ala	Pro	Glu	Phe
91	GAA	AAG	GAT	CTT	CTC	ATT	CAG	AGA	CTC	AAT	TGG	ATG	CTA	TGG	GTG
31	E	K	D	L	L	I	Q	R	L	N	W	M	L	W	V
31	Glu	Lys	Asp	Leu	Leu	Ile	Gln	Arg	Leu	Asn	Trp	Met	Leu	Trp	Val
136	ATC	GAT	GAA	TGC	TTC	CGC	GAC	CTC	TGT	TAC	CGT	ACC	GGC	ATC	TGC
46	I	D	E	C	F	R	D	L	C	Y	R	T	G	I	C
46	Ile	Asp	Glu	Cys	Phe	Arg	Asp	Leu	Cys	Tyr	Arg	Thr	Gly	Ile	Cys
181	AAG	GGT	ATT	CTA	GAG	CCC	GCT	GCT	ATT	TTT	CAT	CTG	AAA	CTA	CCA
61	K	G	I	L	E	P	A	A	I	F	H	L	K	L	P
61	Lys	Gly	Ile	Leu	Glu	Pro	Ala	Ala	Ile	Phe	His	Leu	Lys	Leu	Pro
226	GCC	ATC	AAC	GAT	ACT	GAT	CAC	TGC	GGG	TTA	ATA	GGA	TTT	AAT	GAG
76	A	I	N	D	T	D	H	C	G	L	I	G	F	N	E
76	Ala	Ile	Asn	Asp	Thr	Asp	His	Cys	Gly	Leu	Ile	Gly	Phe	Asn	Glu
271	ACT	AGC	TGC	CTT	AAA	AAG	CTC	GCC	GAT	GGC	TTT	TTT	GAA	TTC	GAG
91	T	S	C	L	K	K	L	A	D	G	F	F	E	F	E
91	Thr	Ser	Cys	Leu	Lys	Lys	Leu	Ala	Asp	Gly	Phe	Phe	Glu	Phe	Glu
316	GTG	TTG	TTT	AAG	TTT	TTA	ACG	ACG	GAG	TTT	GGA	AAA	TCA	GTG	ATA
106	V	L	F	K	F	L	T	T	E	F	G	K	S	V	I
106	Val	Leu	Phe	Lys	Phe	Leu	Thr	Thr	Glu	Phe	Gly	Lys	Ser	Val	Ile
361	AAC	GTG	GAC	GTC	ATG	GAG	CTT	CTG	ACG	AAG	ACC	TTA	GGA	TGG	GAC
121	N	V	D	V	M	E	L	L	T	K	T	L	G	W	D
121	Asn	Val	Asp	Val	Met	Glu	Leu	Leu	Thr	Lys	Thr	Leu	Gly	Trp	Asp
406	ATA	CAG	GAA	GAG	CTC	AAT	AAG	CTG	ACT	AAG	ACG	CAC	TAC	AGT	CCA
136	I	Q	E	E	L	N	K	L	T	K	T	H	Y	S	P
136	Ile	Gln	Glu	Glu	Leu	Asn	Lys	Leu	Thr	Lys	Thr	His	Tyr	Ser	Pro
451	CCC	AAA	TTT	GAC	CGC	GGT	CTA	TTA	GGG	AGG	CTT	CAG	GGA	CTT	AAG
151	P	K	F	D	R	G	L	L	G	R	L	Q	G	L	K
151	Pro	Lys	Phe	Asp	Arg	Gly	Leu	Leu	Gly	Arg	Leu	Gln	Gly	Leu	Lys
496	TAT	TGG	GTG	AGA	CAC	TTT	GCT	TCG	TTT	TAT	GTT	CTG	AGT	GCA	ATG
166	Y	W	V	R	H	F	A	S	F	Y	V	L	S	A	M
166	Tyr	Trp	Val	Arg	His	Phe	Ala	Ser	Phe	Tyr	Val	Leu	Ser	Ala	Met

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541 GAA AAG TTT GCA GGT CAA GCG GTG CGT GTT TTG GAC TCT ATC CCA
181 E K F A G Q A V R V L D S I P
181 Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp Ser Ile Pro

586 GAC GTG ACT CCT GAC GTC CAC GAT AAG
196 D V T P D V H D K
196 Asp Val Thr Pro Asp Val His Asp Lys